HLA-DQA1*05:01/HLA-DQB1*02:01 and HLA-DQA1*05:05/HLA-DQB1*03:01.

12. The method of claim **1**, wherein the machine learning HLA-peptide binding prediction model has a positive predictive value (PPV) of at least 0.1 when amino acid information of a plurality of test peptide sequences are processed to generate a plurality of test binding predictions according to a binding PPV determination method, wherein each test binding prediction is indicative of a likelihood that the one or more proteins encoded by a class II HLA allele of a cell of the subject binds to a given test peptide sequence of the plurality of test peptide sequences, wherein the plurality of test peptide sequences comprises at least 20 test peptide sequences comprising

(i) at least one hit peptide sequence identified by mass spectrometry to be presented by an HLA protein expressed in cells and

(ii) at least 19 decoy peptide sequences contained within a protein comprising at least one peptide sequence identified by mass spectrometry to be presented by an HLA protein expressed in cells, such as a single HLA protein expressed in cells,

wherein the plurality of test peptide sequences comprises a ratio of 1:19 of the at least one hit peptide sequence to the at least 19 decoy peptide sequences and a top 0.5% of the plurality of test peptide sequences are predicted to bind to the HLA protein expressed in cells by the machine learning HLA-peptide presentation prediction model.

13. The method of claim **1**, wherein the method comprises obtaining a plurality of polynucleotide sequences of the subject by genome, transcriptome, or exome sequencing, wherein the plurality of polynucleotide sequences encode the plurality of candidate peptide sequences.

14. The method of claim **13**, wherein the genome, transcriptome or exome sequencing is whole genome sequencing, whole transcriptome, or whole exome sequencing.

15. The method of claim **1**, wherein the method comprises selecting one or more epitope sequences of the plurality of candidate peptide sequences for preparing a pharmaceutical composition, wherein the plurality of candidate peptide sequences have been ranked based on the plurality of presentation predictions.

16. The method of claim **15**, wherein each of the one or more selected epitope sequences binds to a protein encoded by a class II HLA allele of a cell of the subject with an IC50 of 500 nM or less, or a predict-ed IC50 of 500 nM or less.

17. The method of claim **15**, wherein the method further comprises preparing the pharmaceutical composition, wherein the pharmaceutical composition comprises one or more polypeptides comprising at least two of the selected epitope sequences or one or more polynucleotides encoding the at least two of the selected epitope sequences.

18. The method of claim **15**, wherein the method further comprises administering the pharmaceutical composition to the subject, wherein the pharmaceutical composition comprises one or more polypeptides comprising at least one of the selected epitope sequences or one or more polynucleotides encoding at least one of the selected epitope sequences.

19. The method of claim **18**, wherein the pharmaceutical composition further comprises an adjuvant.

20. The method of claim **18**, wherein the pharmaceutical composition elicits a CD4+ T cell response and/or a CD8+ T cell response in the subject.

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